



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:38 PM GMT

PDB ID : 3UJ0
Title : Crystal structure of the inositol 1,4,5-trisphosphate receptor with ligand bound form.
Authors : Ikura, M.; Seo, M.D.; Ishiyama, N.; Stathopulos, P.
Deposited on : 2011-11-07
Resolution : 3.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

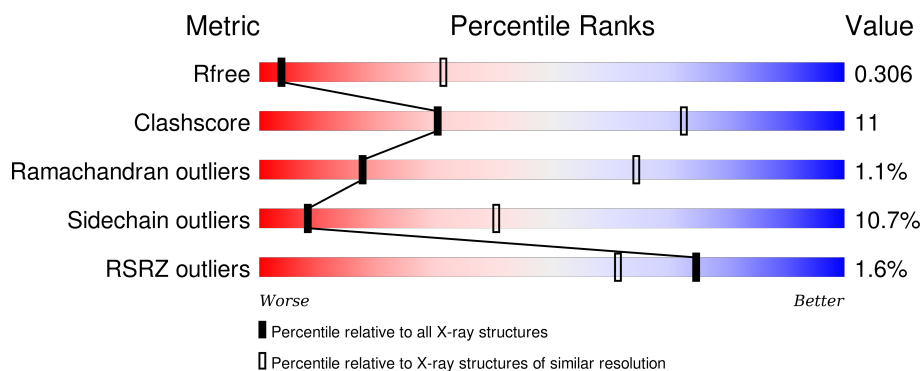
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

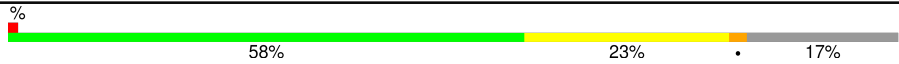

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1408 (3.80-3.40)
Clashscore	102246	1010 (3.74-3.46)
Ramachandran outliers	100387	1007 (3.76-3.44)
Sidechain outliers	100360	1007 (3.76-3.44)
RSRZ outliers	91569	1003 (3.78-3.42)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	604	
1	B	604	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7779 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Inositol 1,4,5-trisphosphate receptor type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	502	Total	C	N	O	S	0	0	0
			3850	2438	681	724	7			
1	B	502	Total	C	N	O	S	0	0	0
			3872	2453	687	725	7			

There are 26 discrepancies between the modelled and reference sequences:

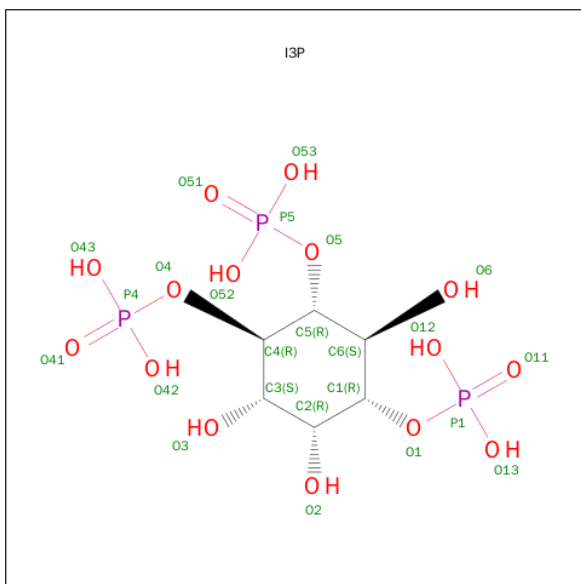
Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ALA	CYS	engineered mutation	UNP P29994
A	37	ALA	CYS	engineered mutation	UNP P29994
A	56	ALA	CYS	engineered mutation	UNP P29994
A	61	ALA	CYS	engineered mutation	UNP P29994
A	206	ALA	CYS	engineered mutation	UNP P29994
A	214	ALA	CYS	engineered mutation	UNP P29994
A	253	ALA	CYS	engineered mutation	UNP P29994
A	292	ALA	CYS	engineered mutation	UNP P29994
A	326	ALA	CYS	engineered mutation	UNP P29994
A	394	ALA	CYS	engineered mutation	UNP P29994
A	530	ALA	CYS	engineered mutation	UNP P29994
A	553	ALA	CYS	engineered mutation	UNP P29994
A	556	ALA	CYS	engineered mutation	UNP P29994
B	15	ALA	CYS	engineered mutation	UNP P29994
B	37	ALA	CYS	engineered mutation	UNP P29994
B	56	ALA	CYS	engineered mutation	UNP P29994
B	61	ALA	CYS	engineered mutation	UNP P29994
B	206	ALA	CYS	engineered mutation	UNP P29994
B	214	ALA	CYS	engineered mutation	UNP P29994
B	253	ALA	CYS	engineered mutation	UNP P29994
B	292	ALA	CYS	engineered mutation	UNP P29994
B	326	ALA	CYS	engineered mutation	UNP P29994
B	394	ALA	CYS	engineered mutation	UNP P29994
B	530	ALA	CYS	engineered mutation	UNP P29994
B	553	ALA	CYS	engineered mutation	UNP P29994

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	556	ALA	CYS	engineered mutation	UNP P29994

- Molecule 2 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (three-letter code: I3P) (formula: $C_6H_{15}O_{15}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			24	6	15	3		
2	B	1	Total	C	O	P	0	0
			24	6	15	3		

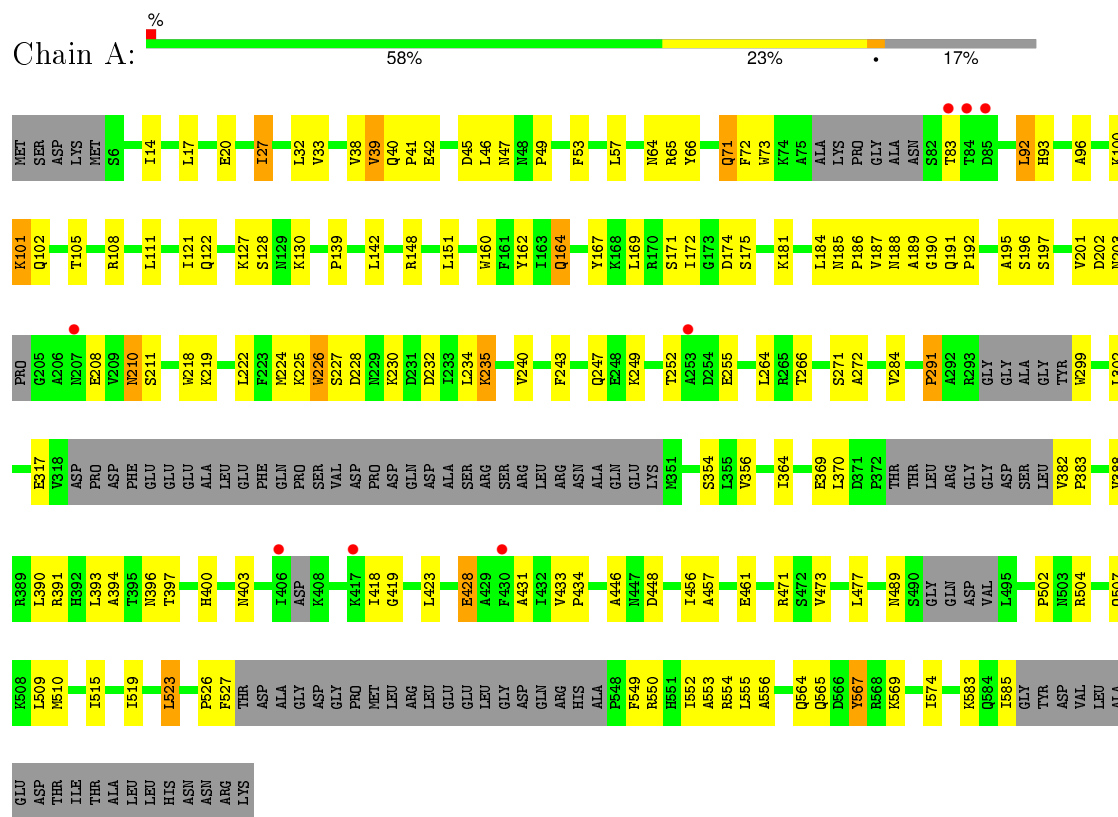
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	O	0	0
			5	5		
3	B	4	Total	O	0	0
			4	4		

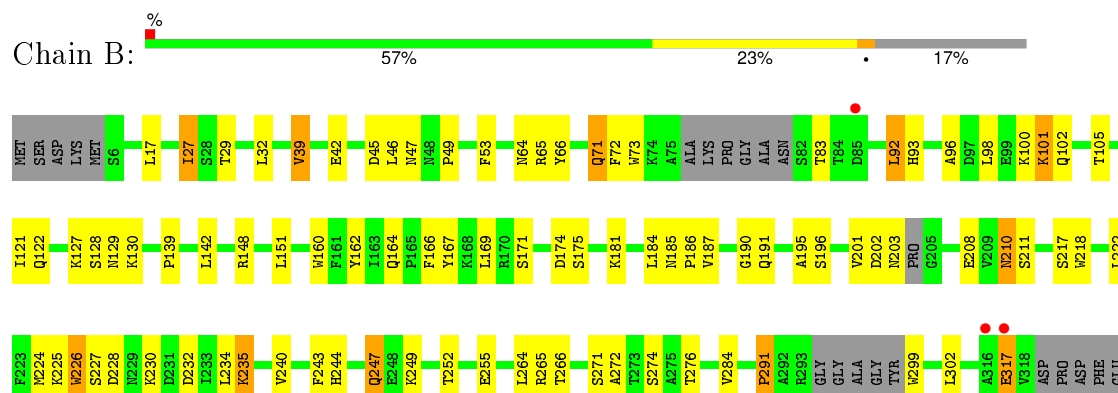
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Inositol 1,4,5-trisphosphate receptor type 1



- Molecule 1: Inositol 1,4,5-trisphosphate receptor type 1





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	189.17Å 78.72Å 134.11Å 90.00° 124.49° 90.00°	Depositor
Resolution (Å)	50.00 – 3.60 44.42 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-3.60) 99.6 (44.42-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.258 , 0.308 0.247 , 0.306	Depositor DCC
R_{free} test set	981 reflections (5.44%)	DCC
Wilson B-factor (Å ²)	110.6	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 91.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	4 of 19012 reflections (0.021%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7779	wwPDB-VP
Average B, all atoms (Å ²)	133.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.80% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: I3P

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.48	2/3920 (0.1%)	0.57	0/5309
1	B	0.48	2/3943 (0.1%)	0.57	0/5336
All	All	0.48	4/7863 (0.1%)	0.57	0/10645

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	73	TRP	CD2-CE2	5.18	1.47	1.41
1	A	73	TRP	CD2-CE2	5.15	1.47	1.41
1	A	226	TRP	CD2-CE2	5.05	1.47	1.41
1	B	226	TRP	CD2-CE2	5.03	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3850	0	3728	89	0
1	B	3872	0	3766	81	0
2	A	24	0	9	0	0
2	B	24	0	9	2	0
3	A	5	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	4	0	0	0	0
All	All	7779	0	7512	168	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (168) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:GLN:HB3	1:A:574:ILE:HD12	1.53	0.90
1:B:196:SER:HB2	1:B:208:GLU:O	1.76	0.86
1:A:196:SER:HB2	1:A:208:GLU:O	1.77	0.85
1:A:49:PRO:HG2	1:A:291:PRO:HG2	1.59	0.83
1:B:171:SER:O	1:B:174:ASP:HB2	1.80	0.82
1:A:171:SER:O	1:A:174:ASP:HB2	1.81	0.79
1:B:234:LEU:HD11	1:B:284:VAL:HG21	1.66	0.78
1:A:567:TYR:HE2	1:A:569:LYS:HB3	1.50	0.77
1:A:567:TYR:CE2	1:A:569:LYS:HB3	2.21	0.75
1:A:64:ASN:HB2	1:A:122:GLN:HE22	1.51	0.74
1:A:64:ASN:HB2	1:A:122:GLN:NE2	2.04	0.73
1:B:354:SER:HA	1:B:419:GLY:HA2	1.71	0.73
1:A:354:SER:HA	1:A:419:GLY:HA2	1.71	0.72
1:B:45:ASP:CG	1:B:46:LEU:H	1.93	0.72
1:A:230:LYS:HA	1:A:232:ASP:H	1.56	0.70
1:A:33:VAL:HG23	1:A:448:ASP:HB3	1.73	0.70
1:A:167:TYR:HE1	1:A:181:LYS:HD2	1.55	0.70
1:B:49:PRO:HG2	1:B:291:PRO:HG2	1.73	0.70
1:B:64:ASN:HB2	1:B:122:GLN:HE22	1.55	0.70
1:B:230:LYS:HA	1:B:232:ASP:H	1.55	0.69
1:B:240:VAL:HG12	1:B:434:PRO:HA	1.75	0.69
1:A:234:LEU:HD11	1:A:284:VAL:HG21	1.74	0.69
2:B:1000:I3P:H3	2:B:1000:I3P:O42	1.93	0.68
1:B:64:ASN:HB2	1:B:122:GLN:NE2	2.08	0.68
1:B:564:GLN:HB3	1:B:574:ILE:HD12	1.76	0.67
1:B:230:LYS:HA	1:B:232:ASP:N	2.10	0.67
1:A:230:LYS:HA	1:A:232:ASP:N	2.11	0.66
1:A:240:VAL:HG12	1:A:434:PRO:HA	1.78	0.65
1:B:567:TYR:CE2	1:B:569:LYS:HB3	2.32	0.65
1:B:45:ASP:CG	1:B:46:LEU:N	2.49	0.65
1:A:45:ASP:CG	1:A:46:LEU:H	1.99	0.64
1:B:167:TYR:HE1	1:B:181:LYS:HD2	1.61	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:ASP:CG	1:A:46:LEU:N	2.53	0.62
1:B:400:HIS:HA	1:B:428:GLU:HG2	1.82	0.62
1:A:456:ILE:HG12	1:A:473:VAL:HG21	1.82	0.62
1:B:370:LEU:HD22	1:B:388:VAL:HG21	1.84	0.60
1:A:400:HIS:HA	1:A:428:GLU:HG2	1.82	0.60
1:A:391:ARG:HH11	1:A:396:ASN:ND2	1.99	0.60
1:A:264:LEU:HG	1:A:418:ILE:HD11	1.84	0.59
1:B:482:TYR:CD1	1:B:487:GLY:HA2	2.37	0.59
1:A:299:TRP:HB2	1:A:382:VAL:N	2.17	0.59
1:B:196:SER:CB	1:B:208:GLU:O	2.51	0.59
1:B:299:TRP:HB2	1:B:382:VAL:N	2.18	0.59
1:B:391:ARG:HH11	1:B:396:ASN:ND2	2.01	0.58
1:A:196:SER:CB	1:A:208:GLU:O	2.49	0.58
1:A:510:MET:HA	1:A:515:ILE:HG13	1.85	0.58
1:A:39:VAL:HG21	1:A:195:ALA:HB1	1.85	0.58
1:B:32:LEU:HD21	1:B:128:SER:HA	1.86	0.58
1:A:370:LEU:HD22	1:A:388:VAL:HG21	1.86	0.58
1:B:549:PHE:HD1	1:B:552:ILE:HB	1.69	0.58
1:A:504:ARG:HA	1:A:507:GLN:HE21	1.69	0.57
1:B:264:LEU:HG	1:B:418:ILE:HD11	1.86	0.57
1:B:71:GLN:HB3	1:B:92:LEU:CD2	2.35	0.57
1:B:27:ILE:HG12	1:B:218:TRP:CZ3	2.40	0.57
1:A:27:ILE:HG12	1:A:218:TRP:CZ3	2.40	0.57
1:A:391:ARG:HH11	1:A:396:ASN:HD22	1.51	0.56
1:B:39:VAL:HG21	1:B:195:ALA:HB1	1.87	0.56
1:A:364:ILE:HG22	1:A:394:ALA:HB2	1.87	0.56
1:A:162:TYR:CE1	1:A:187:VAL:HA	2.40	0.56
1:B:162:TYR:CE1	1:B:187:VAL:HA	2.41	0.56
1:B:364:ILE:HG22	1:B:394:ALA:HB2	1.90	0.54
1:A:191:GLN:O	1:A:211:SER:OG	2.25	0.54
1:B:391:ARG:HH11	1:B:396:ASN:HD22	1.55	0.54
1:A:139:PRO:O	1:A:148:ARG:HB2	2.08	0.54
1:A:32:LEU:HD21	1:A:128:SER:HA	1.89	0.53
1:B:96:ALA:O	1:B:100:LYS:HB2	2.09	0.53
1:A:96:ALA:O	1:A:100:LYS:HB2	2.09	0.53
1:B:243:PHE:HB3	1:B:431:ALA:HB3	1.90	0.52
1:A:502:PRO:HG3	1:A:565:GLN:HG2	1.92	0.52
1:B:139:PRO:O	1:B:148:ARG:HB2	2.10	0.52
1:A:243:PHE:HB3	1:A:431:ALA:HB3	1.92	0.52
1:B:482:TYR:CE1	1:B:487:GLY:HA2	2.45	0.51
1:A:71:GLN:HB3	1:A:92:LEU:CD2	2.40	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:VAL:HG23	1:A:448:ASP:CB	2.41	0.51
1:A:549:PHE:HA	1:A:552:ILE:HD12	1.92	0.51
1:B:249:LYS:HZ2	1:B:266:THR:HA	1.77	0.50
1:A:66:TYR:HE1	1:A:122:GLN:HE22	1.60	0.50
1:A:33:VAL:CG2	1:A:448:ASP:HB3	2.39	0.50
1:A:210:ASN:C	1:A:210:ASN:HD22	2.15	0.50
1:B:441:ARG:HA	1:B:444:ASP:HB2	1.94	0.50
1:B:456:ILE:HG12	1:B:473:VAL:HG21	1.93	0.49
1:A:519:ILE:O	1:A:523:LEU:HD22	2.13	0.49
1:A:235:LYS:HB2	3:A:607:HOH:O	2.11	0.49
1:A:167:TYR:CE1	1:A:181:LYS:HD2	2.44	0.48
1:B:210:ASN:HD22	1:B:210:ASN:C	2.16	0.48
1:B:191:GLN:O	1:B:211:SER:OG	2.27	0.48
1:B:443:LEU:O	1:B:447:ASN:HB2	2.14	0.48
1:A:122:GLN:HE21	1:A:160:TRP:HD1	1.61	0.48
1:A:567:TYR:HE2	1:A:569:LYS:CB	2.25	0.48
1:A:477:LEU:HB3	1:A:555:LEU:HD22	1.95	0.47
1:A:564:GLN:HB3	1:A:574:ILE:CD1	2.36	0.47
1:A:65:ARG:NH2	1:B:175:SER:OG	2.41	0.47
1:A:175:SER:HG	1:B:65:ARG:HH21	1.63	0.47
1:B:481:VAL:HG23	1:B:559:VAL:HG22	1.97	0.47
1:B:391:ARG:NH2	1:B:393:LEU:HD12	2.30	0.47
1:B:225:LYS:C	1:B:227:SER:H	2.18	0.47
1:A:249:LYS:HZ2	1:A:266:THR:HA	1.79	0.47
1:B:202:ASP:OD2	1:B:203:ASN:ND2	2.48	0.46
1:A:108:ARG:O	1:A:111:LEU:HB2	2.15	0.46
1:B:122:GLN:HE21	1:B:160:TRP:HD1	1.62	0.46
1:A:235:LYS:HA	1:A:235:LYS:HD3	1.77	0.46
1:A:507:GLN:C	1:A:509:LEU:H	2.18	0.46
1:A:32:LEU:N	1:A:448:ASP:OD2	2.47	0.46
1:A:446:ALA:HB1	1:A:515:ILE:HD11	1.97	0.46
1:B:32:LEU:N	1:B:448:ASP:OD2	2.46	0.45
1:B:66:TYR:HE1	1:B:122:GLN:HE22	1.64	0.45
1:A:225:LYS:C	1:A:227:SER:H	2.20	0.45
1:A:72:PHE:CE1	1:A:93:HIS:HB2	2.50	0.45
1:A:457:ALA:O	1:A:461:GLU:HB2	2.17	0.45
1:B:477:LEU:HA	1:B:480:LEU:HD12	1.99	0.45
1:A:164:GLN:HB3	1:A:164:GLN:HE21	1.65	0.45
1:A:549:PHE:HD1	1:A:553:ALA:HB3	1.81	0.45
1:A:175:SER:OG	1:B:65:ARG:NH2	2.43	0.45
1:B:72:PHE:CE1	1:B:93:HIS:HB2	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:456:ILE:HG21	1:A:473:VAL:HG21	1.98	0.44
1:A:391:ARG:NH2	1:A:393:LEU:HD12	2.33	0.44
1:B:567:TYR:HE2	1:B:569:LYS:HB3	1.81	0.44
1:A:17:LEU:CD2	1:A:184:LEU:HD11	2.48	0.44
1:B:224:MET:SD	1:B:228:ASP:HB3	2.58	0.44
1:A:243:PHE:HZ	1:A:272:ALA:HB1	1.81	0.44
1:A:264:LEU:HG	1:A:418:ILE:CD1	2.47	0.44
1:A:519:ILE:HG23	1:A:556:ALA:HB1	1.99	0.44
1:A:456:ILE:HG12	1:A:473:VAL:CG2	2.47	0.44
1:B:47:ASN:O	1:B:49:PRO:HD3	2.17	0.44
1:A:17:LEU:HD23	1:A:184:LEU:HD11	1.99	0.44
1:B:436:SER:OG	1:B:439:GLU:HB2	2.17	0.44
1:A:130:LYS:HD2	1:A:151:LEU:HB3	2.00	0.43
1:B:460:LEU:HD13	1:B:465:ILE:HG23	2.00	0.43
1:B:506:ARG:O	1:B:510:MET:HG2	2.18	0.43
1:B:17:LEU:HD23	1:B:184:LEU:HD11	2.00	0.43
1:B:364:ILE:HG22	1:B:364:ILE:O	2.19	0.43
1:B:554:ARG:H	1:B:554:ARG:HG2	1.50	0.43
1:B:244:HIS:CD2	1:B:247:GLN:H	2.37	0.43
1:B:129:ASN:HB2	1:B:441:ARG:NH1	2.33	0.43
1:A:47:ASN:O	1:A:49:PRO:HD3	2.19	0.42
1:B:243:PHE:HZ	1:B:272:ALA:HB1	1.84	0.42
1:A:188:ASN:O	1:A:190:GLY:N	2.52	0.42
1:A:196:SER:OG	1:A:197:SER:N	2.53	0.42
1:B:130:LYS:HD2	1:B:151:LEU:HB3	2.01	0.42
1:B:504:ARG:HA	1:B:507:GLN:HE21	1.84	0.42
1:A:202:ASP:OD2	1:A:203:ASN:ND2	2.52	0.42
1:B:264:LEU:HG	1:B:418:ILE:CD1	2.48	0.42
1:A:101:LYS:HD2	1:A:101:LYS:C	2.40	0.42
1:A:20:GLU:OE1	1:A:219:LYS:HB2	2.19	0.42
1:B:186:PRO:HG2	1:B:190:GLY:O	2.20	0.42
1:A:186:PRO:HD2	1:A:192:PRO:HA	2.02	0.42
1:B:166:PHE:CD1	1:B:217:SER:HB3	2.55	0.42
1:B:29:THR:HG22	1:B:151:LEU:CD1	2.50	0.42
1:B:388:VAL:HG22	1:B:432:ILE:HD11	2.01	0.42
1:A:369:GLU:CD	1:A:391:ARG:HH21	2.23	0.42
1:A:40:GLN:HA	1:A:41:PRO:HD3	1.91	0.41
1:B:167:TYR:CE1	1:B:181:LYS:HD2	2.50	0.41
1:B:369:GLU:CD	1:B:391:ARG:HH21	2.23	0.41
1:B:235:LYS:HA	1:B:235:LYS:HD3	1.79	0.41
1:B:317:GLU:HA	1:B:353:TYR:HD2	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:SER:C	1:B:276:THR:H	2.24	0.41
1:B:388:VAL:CG2	1:B:432:ILE:HD11	2.50	0.41
1:B:98:LEU:O	1:B:101:LYS:HG3	2.20	0.41
1:A:14:ILE:HG22	1:A:57:LEU:HD22	2.03	0.41
1:A:186:PRO:HG2	1:A:190:GLY:O	2.21	0.41
1:B:583:LYS:HA	1:B:583:LYS:HD3	1.88	0.41
1:B:17:LEU:CD2	1:B:184:LEU:HD11	2.52	0.40
1:A:162:TYR:HE1	1:A:187:VAL:HA	1.86	0.40
1:A:553:ALA:HA	1:A:554:ARG:HA	1.83	0.40
1:A:57:LEU:HA	1:A:57:LEU:HD23	1.75	0.40
1:A:224:MET:SD	1:A:228:ASP:HB3	2.62	0.40
1:A:128:SER:HB2	1:A:130:LYS:HE3	2.02	0.40
1:B:265:ARG:NH2	2:B:1000:I3P:O43	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	484/604 (80%)	420 (87%)	57 (12%)	7 (1%)	14	59
1	B	484/604 (80%)	423 (87%)	57 (12%)	4 (1%)	24	69
All	All	968/1208 (80%)	843 (87%)	114 (12%)	11 (1%)	17	64

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	550	ARG
1	A	226	TRP
1	B	226	TRP
1	A	53	PHE
1	A	189	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	526	PRO
1	B	53	PHE
1	B	291	PRO
1	A	291	PRO
1	B	383	PRO
1	A	383	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	399/520 (77%)	358 (90%)	41 (10%)	9	42
1	B	403/520 (78%)	358 (89%)	45 (11%)	7	38
All	All	802/1040 (77%)	716 (89%)	86 (11%)	8	40

All (86) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ILE
1	A	38	VAL
1	A	39	VAL
1	A	42	GLU
1	A	71	GLN
1	A	83	THR
1	A	92	LEU
1	A	101	LYS
1	A	102	GLN
1	A	105	THR
1	A	121	ILE
1	A	127	LYS
1	A	142	LEU
1	A	164	GLN
1	A	169	LEU
1	A	172	ILE
1	A	185	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	201	VAL
1	A	210	ASN
1	A	222	LEU
1	A	235	LYS
1	A	247	GLN
1	A	252	THR
1	A	255	GLU
1	A	271	SER
1	A	302	LEU
1	A	317	GLU
1	A	356	VAL
1	A	390	LEU
1	A	397	THR
1	A	403	ASN
1	A	423	LEU
1	A	428	GLU
1	A	433	VAL
1	A	471	ARG
1	A	489	ASN
1	A	523	LEU
1	A	527	PHE
1	A	567	TYR
1	A	583	LYS
1	A	585	ILE
1	B	27	ILE
1	B	39	VAL
1	B	42	GLU
1	B	71	GLN
1	B	83	THR
1	B	92	LEU
1	B	101	LYS
1	B	102	GLN
1	B	105	THR
1	B	121	ILE
1	B	127	LYS
1	B	142	LEU
1	B	164	GLN
1	B	169	LEU
1	B	185	ASN
1	B	201	VAL
1	B	210	ASN
1	B	222	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	235	LYS
1	B	247	GLN
1	B	252	THR
1	B	255	GLU
1	B	271	SER
1	B	302	LEU
1	B	317	GLU
1	B	356	VAL
1	B	390	LEU
1	B	397	THR
1	B	403	ASN
1	B	423	LEU
1	B	428	GLU
1	B	433	VAL
1	B	451	LYS
1	B	471	ARG
1	B	482	TYR
1	B	489	ASN
1	B	490	SER
1	B	499	PHE
1	B	515	ILE
1	B	523	LEU
1	B	527	PHE
1	B	554	ARG
1	B	555	LEU
1	B	567	TYR
1	B	581	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	GLN
1	A	164	GLN
1	A	185	ASN
1	A	191	GLN
1	A	207	ASN
1	A	210	ASN
1	A	215	ASN
1	A	270	GLN
1	A	307	HIS
1	A	396	ASN
1	A	403	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	507	GLN
1	A	551	HIS
1	A	564	GLN
1	B	122	GLN
1	B	164	GLN
1	B	185	ASN
1	B	194	HIS
1	B	207	ASN
1	B	210	ASN
1	B	215	ASN
1	B	244	HIS
1	B	270	GLN
1	B	307	HIS
1	B	396	ASN
1	B	403	ASN
1	B	468	ASN
1	B	507	GLN
1	B	513	GLN
1	B	524	GLN
1	B	551	HIS
1	B	564	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link

column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	I3P	A	1000	-	24,24,24	0.56	0	33,39,39	1.06	1 (3%)
2	I3P	B	1000	-	24,24,24	0.57	0	33,39,39	1.00	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	I3P	A	1000	-	-	0/15/39/39	0/1/1/1
2	I3P	B	1000	-	-	0/15/39/39	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	1000	I3P	C3-C2-C1	2.05	114.09	109.60

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1000	I3P	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	502/604 (83%)	0.05	8 (1%) 74 61	80, 130, 185, 208	0
1	B	502/604 (83%)	0.01	8 (1%) 74 61	78, 130, 182, 210	0
All	All	1004/1208 (83%)	0.03	16 (1%) 74 61	78, 130, 184, 210	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	253	ALA	3.6
1	B	316	ALA	3.6
1	A	85	ASP	3.5
1	B	457	ALA	2.8
1	A	83	THR	2.6
1	B	85	ASP	2.6
1	A	417	LYS	2.5
1	B	317	GLU	2.4
1	A	84	THR	2.2
1	A	406	ILE	2.2
1	B	554	ARG	2.1
1	B	417	LYS	2.1
1	B	460	LEU	2.1
1	A	430	PHE	2.1
1	B	430	PHE	2.1
1	A	207	ASN	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	I3P	A	1000	24/24	0.91	0.17	-0.58	136,156,165,168	0
2	I3P	B	1000	24/24	0.92	0.13	-1.76	141,148,156,162	0

6.5 Other polymers [i](#)

There are no such residues in this entry.